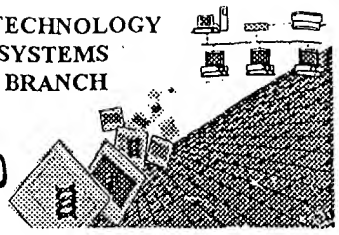
RECEIVED
DEC 2 9 2003
TECH CENTER 1600/2900



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/464,426
Source: 1600
Date Processed by STIC: 12/18/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY** or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: **TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry directly to (EFFECTIVE 12/01/03):** U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/464,426

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 ✓ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/464,426

DATE: 12/18/2003
TIME: 14:49:02

IMPORTANT: see item 4 on Error Summary Sheet

Input Set : A:\ IN01344 - SEQUENCE LISTING\PTO.YF.txt
Output Set: N:\CRF4\12182003\I464426.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
C--> 6 (iii) NUMBER OF SEQUENCES: 4
C--> 0 (vi) CURRENT APPLICATION DATA:
C--> 0 (A) APPLICATION NUMBER: US/09/464,426
C--> 0 (B) FILING DATE: 16-Dec-1999

ERRORED SEQUENCES

Does Not Comply
Diskette Needed

27 (2) INFORMATION FOR SEQ ID NO: 2:
29 (i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 20 base pairs
31 (B) TYPE: nucleic acid
32 (C) STRANDEDNESS: single
33 (D) TOPOLOGY: linear
W--> 35 (ii) MOLECULE TYPE: DNA (oligonucleotide)
39 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
E--> 41 TGCACGGTCT ACGAGACCTC
W--> 42 20
45 (2) INFORMATION FOR SEQ ID NO: 3:
47 (i) SEQUENCE CHARACTERISTICS:
48 (A) LENGTH: 21 base pairs
49 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
51 19
53 (D) TOPOLOGY: linear
W--> 55 (ii) MOLECULE TYPE: DNA (oligonucleotide)
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
E--> 61 CTGTGAGGAA CTACTGTCTT C
W--> 62 21
66 (2) INFORMATION FOR SEQ ID NO: 4:
68 (i) SEQUENCE CHARACTERISTICS:
69 (A) LENGTH: 21 base pairs
70 (B) TYPE: nucleic acid
71 (C) STRANDEDNESS: single
72 (D) TOPOLOGY: linear
W--> 74 (ii) MOLECULE TYPE: DNA (oligonucleotide)
78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
E--> 80 CCCTATCAGG CAGTACCACA A

see pp 2-3 for explanation

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) ~~(i)~~ NUMBER OF SEQUENCES: 4

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGGTCTGCG GAACCGGTGA GT 22

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGCACGGTCT ACGAGACCTC
20 → 20 (see item 1 on Error Summary Sheet)

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(i) APPLICANT:
(ii) TITLE OF INVENTION:
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE:
(B) COMPUTER:
(C) OPERATING SYSTEM:
(D) SOFTWARE:
(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

insert these mandatory headings and responses

delete (19) all page numbers

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGTGAGGAA CTACTGTCTT C
21

21 see item 1

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCTATCAGG CAGTACCACA A

21

VERIFICATION SUMMARY DATE: 12/18/2003
PATENT APPLICATION: **US/09/464,426** TIME: 14:49:03

Input Set : **A:\ IN01344 - SEQUENCE LISTING\PTO.YF.txt**
Output Set: **N:\CRF4\12182003\I464426.raw**

L:6 M:220 C: Keyword misspelled or invalid format, [(iii) NUMBER OF SEQUENCES:]
L:0 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] of (1)
L:0 M:200 E: Mandatory Header Field missing, [(ii) TITLE OF INVENTION:] of (1)
L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(B) STREET:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(C) CITY:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(D) STATE:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(E) COUNTRY:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(F) ZIP:] of (1)(iv)
L:0 M:249 C: Inserted Mandatory Field, [(vi) CURRENT APPLICATION DATA:]
L:0 M:249 C: Inserted Mandatory Field, [(A) APPLICATION NUMBER:]
L:0 M:249 C: Inserted Mandatory Field, [(B) FILING DATE:]
L:16 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:35 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2
L:41 M:254 E: No. of Bases conflict, Input:0 Counted:20 SEQ:2
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:55 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:61 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:3
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:80 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:4